



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:30 AM GMT

PDB ID : 2XAU
Title : CRYSTAL STRUCTURE OF THE PRP43P DEAH-BOX RNA HELICASE
IN COMPLEX WITH ADP
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Deposited on : 2010-03-31
Resolution : 1.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

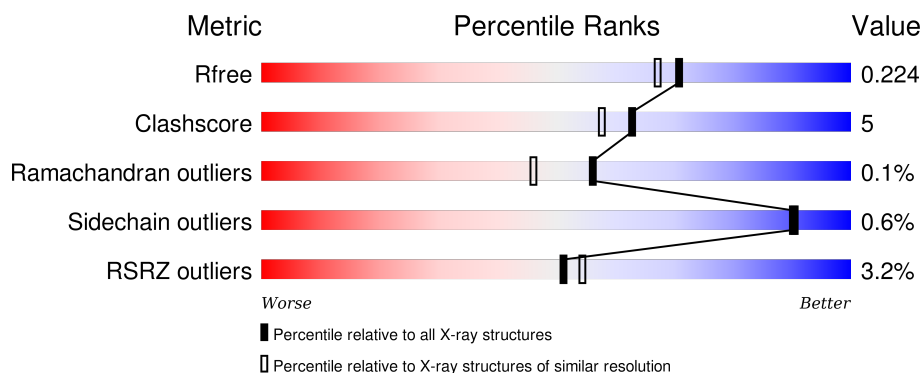
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	773	<div> <div>3%</div> <div>85%</div> <div>11%</div> <div>.</div> </div>
1	B	773	<div> <div>3%</div> <div>84%</div> <div>11%</div> <div>.</div> </div>

2 Entry composition [i](#)

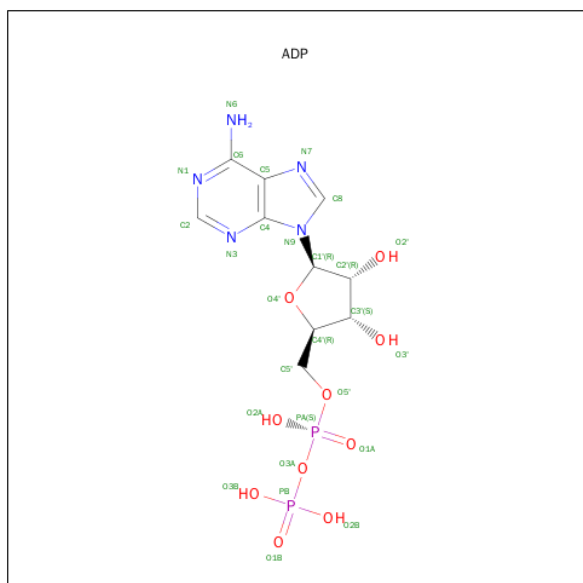
There are 7 unique types of molecules in this entry. The entry contains 13448 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called PRE-MRNA-SPLICING FACTOR ATP-DEPENDENT RNA HELICASE PRP43.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	745	Total	C	N	O	S	0	0	0
			5990	3793	1034	1139	24			
1	B	741	Total	C	N	O	S	0	0	0
			5961	3778	1027	1132	24			

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

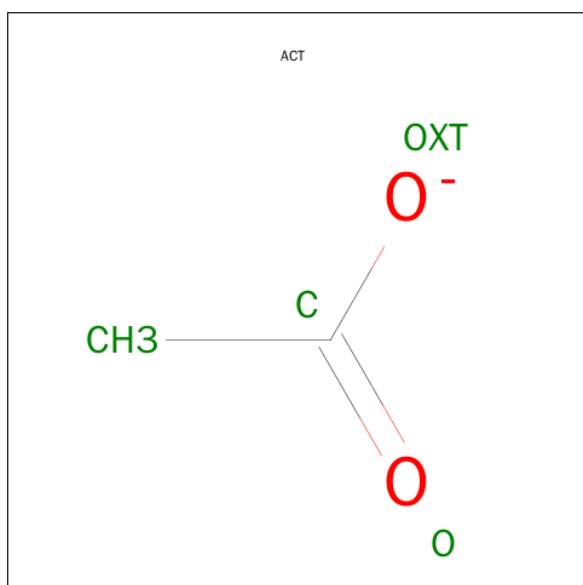
- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0
3	A	1	Total Mg 1 1	0	0

- Molecule 4 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Ni 1 1	0	0
4	A	1	Total Ni 1 1	0	0

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		
6	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	756	Total	O	0	0
			756	756		
7	B	663	Total	O	0	0
			663	663		

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($\text{RSRZ} > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

L738	D561	L285	MET
S739	K562	E281	GLY
K742	R564	E301	S3
I743	F572	E315	E29
K744	F572	G335	L36
E745	V585	L339	P37
K746	V595	V372	S38
V747	I619	S382	G52
ASP	E624	K400	L53
ARG	L634	K404	Q54
LEU	T637	R405	H57
ASN	D638	L406	K70
GLU	R407	R407	I89
LEU	E940	V408	L93
LVS	LVS	E409	V115
GLN	F657	K418	T123
GLY	M658	R427	Q147
LVS	K662	T431	P148
HIS	K662	R432	R149
SER	R664	P433	V156
SER	SER	G434	E170
LVS	GLY	K435	V174
LVS	ALA	A444	S175
HIS	ALA	Q446	I176
HIS	LVS	E448	R177
HIS	G669	V454	F178
HIS	K674	M461	E179
HIS	D675	V466	T186
HIS	D678	M491	Y190
HIS	I681	L472	M191
HIS	L687	D476	T192
HIS	G688	L477	L214
HIS	H689	R493	E219
HIS	D690	E497	R220
HIS	M693	F555	T221
HIS	L701	I556	L230
HIS	S703	R557	L231
HIS	R714	P558	L250
HIS	P715	R557	D251
HIS	E716	T559	A252
HIS	L728	K733	

4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	117.55Å 117.55Å 254.60Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.25 – 1.90 34.40 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.7 (34.25-1.90) 97.6 (34.40-1.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 1.89Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.184 , 0.224 0.184 , 0.224	Depositor DCC
R_{free} test set	7880 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	27.1	Xtriage
Anisotropy	0.187	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 49.3	EDS
Estimated twinning fraction	0.018 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 156817 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13448	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.04% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MG, ACT, ADP, NI

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.82	0/6117	0.79	6/8280 (0.1%)
1	B	0.79	0/6088	0.77	4/8242 (0.0%)
All	All	0.81	0/12205	0.78	10/16522 (0.1%)

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	149	ARG	NE-CZ-NH2	-8.04	116.28	120.30
1	A	177	ARG	NE-CZ-NH2	-7.67	116.46	120.30
1	B	177	ARG	NE-CZ-NH2	-7.33	116.63	120.30
1	A	708	ARG	NE-CZ-NH2	-7.22	116.69	120.30
1	A	708	ARG	NE-CZ-NH1	7.20	123.90	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5990	0	5946	62	0
1	B	5961	0	5921	64	0
2	A	27	0	12	1	0
2	B	27	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	4	0	3	0	0
5	B	4	0	3	0	0
6	A	6	0	8	0	0
6	B	6	0	8	0	0
7	A	756	0	0	5	0
7	B	663	0	0	10	0
All	All	13448	0	11913	126	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 126 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:699:PHE:CE2	1:A:701:LEU:HD21	2.22	0.75
1:B:693:TRP:CD1	1:B:715:PRO:HG3	2.22	0.75
1:A:555:PHE:CZ	1:A:585:VAL:HG11	2.22	0.74
1:B:432:ARG:HB2	1:B:433:PRO:CD	2.19	0.72
1:A:698:GLU:OE1	1:A:708:ARG:HD2	1.90	0.71

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	741/773 (96%)	721 (97%)	20 (3%)	0	100	100
1	B	737/773 (95%)	711 (96%)	25 (3%)	1 (0%)	56	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1478/1546 (96%)	1432 (97%)	45 (3%)	1 (0%)	56 46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	405	ARG

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	660/685 (96%)	656 (99%)	4 (1%)	90 90
1	B	657/685 (96%)	653 (99%)	4 (1%)	90 90
All	All	1317/1370 (96%)	1309 (99%)	8 (1%)	90 90

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	461	ASN
1	B	559	THR
1	B	432	ARG
1	A	414	SER
1	B	281	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ADP	A	1750	3	22,29,29	1.05	1 (4%)	27,45,45	1.81	5 (18%)
5	ACT	A	1753	-	1,3,3	2.02	1 (100%)	0,3,3	0.00	-
6	GOL	A	1754	-	5,5,5	0.04	0	5,5,5	0.57	0
2	ADP	B	1748	3	22,29,29	1.22	3 (13%)	27,45,45	2.01	6 (22%)
5	ACT	B	1751	-	1,3,3	1.78	0	0,3,3	0.00	-
6	GOL	B	1752	-	5,5,5	0.37	0	5,5,5	0.53	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ADP	A	1750	3	-	0/12/32/32	0/3/3/3
5	ACT	A	1753	-	-	0/0/0/0	0/0/0/0
6	GOL	A	1754	-	-	0/4/4/4	0/0/0/0
2	ADP	B	1748	3	-	0/12/32/32	0/3/3/3
5	ACT	B	1751	-	-	0/0/0/0	0/0/0/0
6	GOL	B	1752	-	-	0/4/4/4	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1748	ADP	PB-O2B	-2.35	1.46	1.54
2	A	1750	ADP	C5-N7	-2.03	1.32	1.39
2	B	1748	ADP	PB-O1B	2.01	1.57	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1753	ACT	CH3-C	2.02	1.51	1.48
2	B	1748	ADP	C5-C4	2.66	1.46	1.40

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1748	ADP	N3-C2-N1	-7.76	122.95	128.89
2	A	1750	ADP	N3-C2-N1	-6.42	123.98	128.89
2	A	1750	ADP	O2'-C2'-C3'	-3.75	99.65	111.83
2	B	1748	ADP	O2'-C2'-C3'	-3.43	100.66	111.83
2	B	1748	ADP	O4'-C1'-N9	-2.68	102.48	108.10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1750	ADP	1	0
2	B	1748	ADP	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	745/773 (96%)	0.03	20 (2%) 58 61	14, 27, 51, 83	0
1	B	741/773 (95%)	0.08	27 (3%) 46 50	15, 30, 53, 89	0
All	All	1486/1546 (96%)	0.05	47 (3%) 51 54	14, 29, 52, 89	0

The worst 5 of 47 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	250	LEU	7.4
1	B	405	ARG	6.2
1	B	404	PRO	6.0
1	B	252	ALA	5.9
1	A	405	ARG	5.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	ADP	A	1750	27/27	0.98	0.13	0.35	14,30,39,40	0
6	GOL	A	1754	6/6	0.91	0.10	0.15	29,35,36,38	0
3	MG	A	1751	1/1	0.99	0.13	0.13	16,16,16,16	0
5	ACT	A	1753	4/4	0.98	0.09	-0.26	19,20,20,21	0
3	MG	B	1749	1/1	0.99	0.12	-0.44	17,17,17,17	0
5	ACT	B	1751	4/4	0.96	0.09	-0.60	24,24,25,25	0
2	ADP	B	1748	27/27	0.98	0.10	-1.07	15,27,33,35	0
6	GOL	B	1752	6/6	0.95	0.08	-1.10	35,40,44,45	0
4	NI	B	1750	1/1	0.97	0.04	-	42,42,42,42	1
4	NI	A	1752	1/1	0.98	0.04	-	35,35,35,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.